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Article

Follicular Immune Landscaping Reveals a Distinct Profile of FOXP3^{hi} CD4⁺ T Cells in Treated Compared to Untreated HIV

Short Title: Follicular Immune Landscaping in HIV

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Abstract: Follicular helper CD4⁺ T cells (T_{FH}) are a major cellular pool for the maintenance of HIV reservoir. Therefore, the delineation of the follicular (F)/germinal center (GC) immune landscape will significantly advance our understanding of HIV pathogenesis. We have applied multiplex confocal imaging, in combination with relevant computational tools, to investigate, F/GC *in situ* immune dynamics in viremic (vir-HIV), antiretroviral treated (cART HIV) People Living With HIV (PLWH) and compare them to reactive, non-infected controls. Lymph nodes (LNs) from viremic and cART PLWH could be further grouped based on their T_{FH} cell densities in high-T_{FH} and low-T_{FH} subgroups. These subgroups were also characterized by different *in situ* distribution of PD1^{hi} T_{FH} cells. The significantly accumulated follicular, compared to extrafollicular, FOXP3^{hi} CD4⁺ T cells found in the low-T_{FH} cART-HIV group were characterized by a less scattered *in situ* distribution and strongly correlated with the cell density of CD8⁺ T cells in this group. An inverse correlation between plasma viral load and LN GrzB^{hi}CD8⁺ T and CD16^{hi}CD15^{lo} cells was found. Our data reveal the complex GC immune landscaping in HIV infection and suggest that follicular FOXP3^{hi} CD4⁺ T cells could be negative regulators of T_{FH} cell prevalence in cART-HIV.

Keywords: HIV; germinal center; imaging; CD4 T cells

1. Introduction

Despite the intense research in HIV pathogenesis and cure approaches over the last 40 years, several aspects related to relevant immune cell and viral dynamics are still not well understood. Combination antiretroviral therapy (cART) has extended the life expectancy and improved the quality of life of People Living With HIV (PLWH). Although cART blocks HIV replication, it cannot eradicate the virus[1,2]. Latent infection of resting CD4⁺ T cells provides a mechanism for lifelong persistence of HIV[3]. Integrated HIV DNA can be detected in various blood and non-blood tissues,

but recent evidence indicates that genetically intact proviruses are mainly detected in lymph nodes (LNs)[4]. Chronic HIV infection is characterized by dramatic changes of LN architecture, stromal cell loss and adaptive immune cell composition[5]. Follicular helper CD4⁺ T cells (T_{FH}), that play a pivotal role as mediators of functional B cell responses[6,7], represent a major HIV reservoir within central memory CD4⁺ T cells[8,9]. Non-human primate (NHP) studies have shown accumulation of T_{FH} cells in SIV chronically infected compared to non-infected LNs, a phenotype associated with increased frequency of activated germinal center B cells and SIV-specific antibodies[10]. On the other hand, progression to AIDS (acquired immunodeficiency syndrome, advanced stage of disease) was associated with progressive loss of T_{FH} cells in SIV infected NHP[11]. In addition to T_{FH} and GC B cell altered dynamics, chronic HIV/SIV is also characterized by increased cell density of LN/follicular effector CD8⁺ T cells[12], deregulated immune-regulatory (T_{REG}) and follicular immune-regulatory (T_{FR}) levels[13,14], infiltration of inflammatory cell subsets and excessive fibrosis[5,15]. Foxp3^{hi}CD4⁺ T cells were reported to impair the proliferation and cytokine-releasing capacity of T_{FH} in ex vivo HIV-focused studies[14]. Additionally, IL-10 and CTLA-4 expression of T_{FR} cells were up-regulated in treatment-naïve PLWH[16]. Innate immune cells, which contribute to the adaptive immune responses either by antigen presentation or by secretion of immunomodulatory cytokines[17], play an important role in HIV pathogenesis[18,19] while their role in cure strategies[20] is a field under development.

Several studies have focused on the characterization of LN-derived T cells, mainly using LN-derived cell suspensions and Flow or Mass cytometry-based assays[21] or single cell RNA analysis[22,23]. However, these experimental approaches lack the information of immune cell spatial organization. *In situ* characterization of immune cell types using multiplex imaging methodologies and appropriate cohorts of control and disease samples, can provide important insight into the prevalence, phenotype, and spatial organization of relevant immune cells in HIV that could also indicate possible mechanistic interactions between specific cell types.

Herein, we applied multiplex imaging combined with advanced computational tools for the comprehensive characterization of the immune landscaping in viremic and cART HIV LNs compared to reactive control LNs or tonsils from non-HIV infected individuals. Our results indicate that both viremic and cART HIV LNs can be further grouped based on T_{FH} cell density. These groups exhibited distinct profiles of Foxp3^{hi}CD4⁺ T, Granzyme B (GrzB)^{hi}CD8⁺ T and innate immune cell subsets. Our work points to a possible role of FOXP3^{hi}CD4⁺ T cells as regulators of T_{FH} cells in HIV, particularly in cART individuals. Our neighboring analysis revealed a distinct distribution pattern for both T_{FH} and follicular (F-)FOXP3^{hi}CD4⁺ T between PLWH subgroups as well as compared to non-infected donors.

2. Materials and Methods

2.1. Human Material

The tissue samples used in this study were obtained from i) the Centro de Investigación en Enfermedades Infecciosas (CIENI), Instituto Nacional de Enfermedades Respiratorias (INER) in Mexico City, Mexico (viremic LNs), ii) the University of Washington, Seattle, USA (cART HIV LNs) and iii) the archives of the Institute of Pathology of Lausanne University Hospital, Switzerland (control LNs). Tonsillar tissues were obtained from anonymized children who underwent routine tonsillectomy at the Hospital de l'Enfance of Lausanne. All procedures were in accordance with the Declaration of Helsinki and approved by the appropriate Institutional Review Board/Ethical Committee: i) all tissue samples from PWH were procured with explicit written informed consent from participants prior to donation, adhering strictly to the principles outlined in the Declaration of Helsinki.

2.2. Tissue Processing

Formalin-fixed, paraffin embedded (FFPE) blocks were sequentially cut into 4 µm sections and prepared on Superfrost glass slides (Thermo Scientific, Waltham, MA, Ref. J1800AMNZ), dried overnight at 37°C and stored at 4°C. Before staining, the slides were heated on a metal hotplate (Stretching Table, Medite, Burgdorf, OTS 40.2025, Ref. 9064740715) at 65°C for 20 min. This melting

step ensures proper adherence and deparaffinization of tissue section. Fluorescent multiplex immunohistochemistry (mIHC) staining was performed on the Ventana Discovery Ultra Autostainer from Roche Diagnostics.

2.3. Confocal Imaging Assays

2.3.1. Tissue Staining & Data Acquisition

Tissue sections were sequentially subjected to antibody blocking using the Opal blocking/antibody diluent solution, (ARD1001EA) staining with primary antibodies (details on antibodies, clones and dilutions are listed in Suppl. Table 1), incubation with secondary HRP-labeled antibodies for 16 minutes, detection with optimized fluorescent Opal tyramide signal amplification (TSA) dyes (Opal 7-color Auto-mation IHC kit, from Akoya, Ref. NEL821001KT) and repeated antibody denaturation cycles. Samples were then counterstained with Spectral DAPI from Akoya for 4 min, rinsed in soapy water and mounted using DAKO mounting medium (Dako/Agilent, Santa Clara, CA, USA, Ref. S302380-2).

Images were acquired using a Leica Stellaris 8 SP8 confocal system, equipped with the LAS-X software, at 512 x 512-pixel density and 0.75x optical zoom using a 20x objective (NA), unless otherwise stated. Frame averaging or summing was never used while obtaining the images. At least 70% of each section was imaged, to ensure accurate representation and minimize selection bias. Tissues stained with a single antibody-fluorophore combination were used to create a compensation matrix via the Leica LAS-AF Channel Dye Separation module (Leica Microsystems), which was used to correct fluorophore spillover (when present), as per user's manual.

2.3.2. Quantitative Imaging Analysis (Histocytometry)

Confocal image analysis was performed with Imaris software version 9.9.0 (Bitplane). Quantitative data were generated from the images through histocytometry analysis[24,25], as previously reported. In brief, the Surface Creation module of Imaris was used to generate 3-dimensional segmented surfaces (based on nuclear signal) of spillover corrected images. Data generated from histocytometry such as average voxel intensities for all channels, in addition to volume and sphericity of the 3-dimensional surfaces, were exported in Microsoft Excel format. The files were converted to comma separated value (.CSV) files and the data were imported into FlowJo (version 10) to be further analyzed and quantitated. Well-defined areas devoid of background staining were included in the analysis and data were quantified either as relative frequencies or as cell counts normalized to total follicular area screened. Optimal z-stack settings were applied in all collected images. Maximum Intensity Projections (MIP) are presented throughout the manuscript.

2.3.3. Data analysis-Neighboring Analysis

The distance between relevant cell subsets (CD20^{hi}, PD1^{hi}CD57^{hi/lo} e.t.c) was calculated with python 3.10.9 using the SciPy library[26]. The matrix interaction was created using X and Y coordinates from each cell phenotype and the median distance was extracted. Furthermore, to characterize the probability to observe different patterns of cellular distribution across Regions Of Interest (ROIs) and patients, we study the curves generated from the Ripley's G function and the theoretical Poisson curve using pointpats 2.3.0 (<https://doi.org/10.5281/zenodo.7706219>). The area between the empirical and theoretical Poisson curve was extracted using the NumPy library[27]. ROIs with at least 20 positive cells for each cell subset under investigation were analyzed. The data were presented as i) bar graphs, showing the range of all various distances measured (X axis) and the frequency or count of B cells that fell within each distance range and ii) dot plots, where each dot represents the mean value of the minimum distances between two cell populations for each follicular area.

2.3.4. Viral Load Measurement

The m2000 system (Abbott, Abbot Park, IL, USA) with a detection limit of 40 HIV RNA copies/mL was used to perform automated real-time polymerase chain reaction (PCR) for the determination of HIV plasma viral load (pVL), with a detection limit of 40 HIV RNA copies/mL. Flow cytometry with the AQUIOS Tetra-1 Panel in AQUIOS CL (Beckman Coulter Life Sciences, Indianapolis, IN, USA) was used to determine CD4⁺ T cell counts. All PWLH involved in the current study were infected with clade B HIV.

2.4. Statistical Analysis

For imaging data analysis, the Mann-Whitney test and simple linear regression analysis were used. The p-values Mann-Whitney test were corrected using the False Discovery Rate (FDR) correction test[28] with $q=0.05$, for multiple comparisons (both uncorrected and corrected p values for each figure are shown in Suppl. Table 2). Analysis and graphs were generated using the GraphPad Prism 8.3.0 software. For statistical significance, p value <0.05 was considered.

3. Results

3.1. Similar Profiles of Follicular Helper CD4⁺ T Cell Densities in Viremic and cART HIV LNs

Given the importance of T_{FH} cells for the HIV reservoir maintenance[29] as well as the development of neutralizing antibodies[30], we sought to investigate their in-situ cell density in HIV infected compared to non-infected tissues. We used tonsils and non-infected, cancer free, reactive LNs characterized by follicular hyperplasia as strict control groups (Figure S1, S6). We started our analysis by applying a multiplex imaging assay allowing for the simultaneous detection of main GC B and T cell subsets (Figure 1A). The gating scheme used for the identification and quantitative analysis of corresponding cell subsets by Histocytometry[24,25] is shown (Figure 1B). The in-situ density of CD20^{hi/dim} cells was used for the identification of individual follicular areas (highly enriched in CD20^{hi/dim} cells) as well as the 'total follicular' area (Figure 1B). As expected [5,31], PWLH tissues harbor both 'preserved' as well as 'irregular' follicular structures (Figure 1A and S1B). CD4⁺ T cell subsets within the 'total follicular' area were analyzed based on their expression of PD1 and CD57 (Figure 1B). Preliminary analysis revealed low expression levels of CD4 in certain T_{FH} cells, particularly the ones expressing CD57 (Figure S2A). Several studies have shown that T_{FH} cells express a unique PD1^{hi} phenotype[9,10,32] compared to other CD4⁺ T cells while PD1 expression per cell (judged by Mean Fluorescence Intensity) of follicular CD8⁺ T cells is 4-5 times lower than that of T_{FH}[24]. Therefore, the expression level of PD1 can serve as an *in situ* T_{FH} identifier. To avoid inconsistencies and misinterpretation of our data, especially for the CD57^{hi} T_{FH} cell subset, we chose to directly analyze the PD1^{hi}CD57^{hi/low} cells in GCs (Figure 1B). The gating for setting the threshold of these biomarkers is shown in Figure S2A. Their expression level in extrafollicular areas as well as the manual inspection of their fluorescence intensities in the raw images, was used as a reference to set the cut-off for 'high' values. Back gating of PD1^{hi} and CD57^{hi} cells identified by Histocytometry (shown as spheres) to the original image showed a high concordance between the digitally identified cells and their original counterparts (Figure 1C).

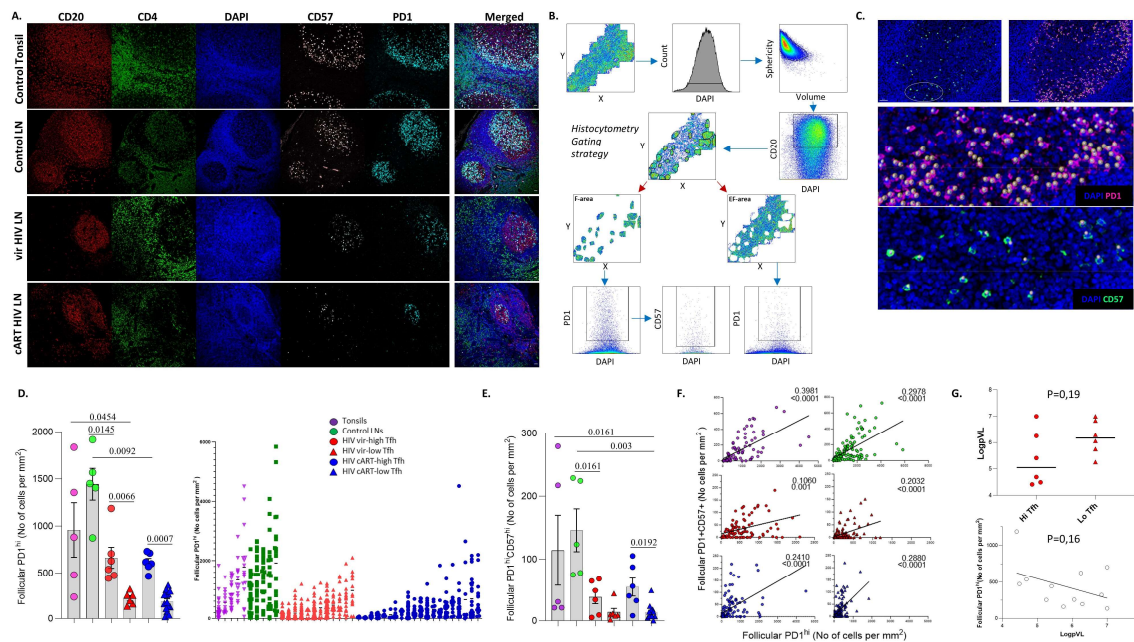


Figure 1. Similar *in situ* cell density of T_H cells in viremic and cART PLWH LNs. (A) Representative examples of CD20 (red), CD4 (green), DAPI (blue), CD57 (grey) and PD1 (cyan) staining pattern from a tonsil and control, viremic and cART HIV LNs (scale bar: 30 μ m). (B) Histocytometry gating strategy used for the sequential identification of T_H cells based on PD1 and CD57 expression after nuclear staining-based cell segmentation on Imaris and FlowJo analysis. F and EF areas were defined based on the density for CD20 signal and manually gated on FlowJo to extract cell counts for specific tissue localities. (C) Histocytometry identified PD1^{hi}CD57^{hi} T_H cells were backgated to the original image using Imaris software. Each sphere represents one cell. (D) Bar graph (left) demonstrating the cell density (normalised per mm² counts) of follicular PD1^{hi} T_H cells in tonsils (N=5), control LNs (N=5), viremic HIV (N=12) and cART HIV LNs (N=20). Viremic and cART were further subdivided based on their T_H counts (HIV vir-high T_H (N=6), HIV vir-low- T_H (N=6), HIV cART-high- T_H (N=6) and HIV cART-low- T_H (N=14)). Each symbol represents one donor. The p values were calculated using the Mann-Whitney test and were corrected using FDR correction with $q=0.05$ (Suppl. Table 2). Dot graph (right) shows the distribution of PD1^{hi} cell densities among samples. Each symbol represents a follicle. (E) Bar graph demonstrating the normalized per mm² numbers of follicular PD1^{hi}CD57^{hi} T_H cells in the same groups/subgroups of samples. (F) Linear regression analysis to address the correlation between PD1^{hi} and PD1^{hi}CD57^{hi} absolute follicular counts among different subgroups. Each symbol represents a follicle. R-squared and p-values are displayed on graphs. (G) Linear regression analysis (lower) to address the correlation between normalized follicular PD1^{hi} counts and blood viral load-pVL. Dot graph (upper) showing the pVL differences (as log scale) between the viremic HIV subgroups.

Calculation of PD1^{hi} cell densities (normalized cell counts per mm²) allowed for further grouping of HIV viremic and cART tissues into two subgroups characterized by significantly different cell densities of PD1^{hi} T_H cells; one with high PD1^{hi} T_H cell densities (hereafter 'high- T_H ') and one with low PD1^{hi} T_H cell densities (hereafter 'low- T_H ') (Figure 1D, left panel). In order to assess the heterogeneous (or not) prevalence of PD1^{hi} T_H cells across an individual tissue, the cell densities of PD1^{hi} T_H per follicle for every tissue were analyzed. A great variability was observed in all tissues, particularly in tonsils and control LNs (Figure 1D, right panel).

CD57, a carbohydrate epitope, marks a T_H cell subset with distinct positioning and function in human LNs[33,34]. As expected [34], the PD1^{hi}CD57^{hi} group represents a subset of T_H cells (Figure 1E). PD1^{hi}CD57^{hi} T_H cells exhibited a similar cell density profile with PD1^{hi} cells (Figure 1E) and heterogeneous prevalence across the tissue (Figure S2B). A strong correlation between PD1^{hi} and PD1^{hi}CD57^{hi} T_H cell densities was found for tonsil, control and cART LNs (Figure 1F). This association was less significant in the high- T_H PLWH viremic subgroup (Figure 1F). Although not statistically

significant, a negative association was observed between the PD1^{hi} T_{FH} cells and pVL in viremic PLWH, as well as a trend for higher pVL in the low-T_{FH} compared to high-T_{FH} viremic PWLH subgroup (Figure 1G, lower and upper panel respectively). Therefore, in agreement with our previous data for viremic SIV infection [10], two subgroups defined by significantly different cell densities of T_{FH} cells were identified in viremic as well as cART HIV LNs.

3.2. A Distinct Positioning Profile of T_{FH} cells in HIV-Infected Compared to Non-Infected Tissues

Next, the spatial positioning of GC B cells and T_{FH} cell subsets was investigated in our tissue cohort. To this end, follicles from all groups, harboring at least 20 cells for each corresponding cell population, were used. The X, Y coordinates of relevant cells were extracted (Figure 2A, upper panel) and digitalized representation of their distribution was generated (Figure 2A, lower panel). Then, the 'G function' parameter, as a surrogate for the dispersion/scattering of a distribution, of a given cell type as well as the mean values of the minimum distances between relevant cell types in individual follicular areas were calculated[35]. An example of follicles with low and high mean distance between CD20^{hi} and PD1^{hi} cells and their associated G parameters is shown (Figure 2B). A similar distribution profile for CD20^{hi} cells, among the tissue subgroups analyzed was detected (Figure 2C). Contrary to B cells, PD1^{hi} cells expressed a significantly higher dispersion in the vir-HIV subgroups compared to control LNs (Figure 2D). Regarding the PD1^{hi} cells distribution of cART tissues, a significant difference was found only between control and low-T_{FH} cART LNs (Figure 2D). Furthermore, a significantly higher dispersion was found in low-T_{FH} compared to high-T_{FH} HIV tissues, in both viremic and cART tissues from PLWH (Figure 2D). A significantly higher mean of minimum distance between CD20^{hi} and PD1^{hi} cells was found in the vir- and cART HIV compared to control tissues (Figure 2E), while no difference was observed among the PLWH subgroups (Figure 2E).

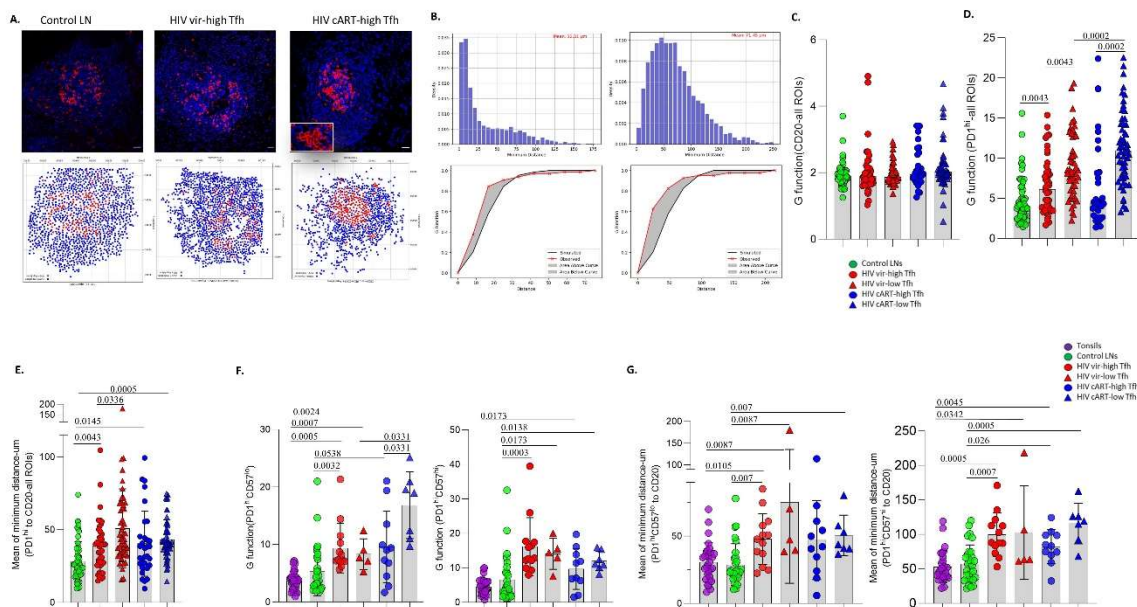


Figure 2. A highly scattered distribution of T_{FH} cells in HIV infected compared to non-infected lymphoid tissues. (A) Representative immunofluorescence images showing the distribution of CD20^{hi} (blue) and PD1^{hi} (red) cells in follicles from one control, one vir-HIV high-T_{FH} and one cART HIV high-T_{FH} tissue. The corresponding digitalized (generated by the Python distance analysis script) images are shown too. (B) The distribution bar graphs for the minimum distance between CD20 and PD1^{hi} cells in two follicular areas (control-left, cART-right) (upper panel). Diagrams showing the theoretical (blue) and experimental (red) Poisson curves for the distribution of PD1^{hi} cells in two follicular areas (control-left, cART-right) (lower panel). Bar graphs showing the G function analysis for total CD20^{hi} (C) and PD1^{hi} T_{FH} cells ((control LNs (N=54), vir-HIV high-T_{FH} (N=42), vir-HIV low-T_{FH} (N=51), cART HIV high-T_{FH} (N=31) and cART HIV low-T_{FH} (N=55)). (D) in individual follicles from

control and infected LNs. (E) The mean of minimum distance values between CD20^{hi} and PD1^{hi} cells in individual follicles from control and infected LNs is shown ((control LNs (N=54), vir- HIV high-T_{FH} (N=42), vir-HIV low-T_{FH} (N=51), cART HIV high-T_{FH} (N=31) and cART HIV low-T_{FH} (N=55)). (F) The G function analysis for PD1^{hi}CD57^{hi} (left) and PD1^{hi}CD57^{lo} (right) T_{FH} cells in tonsils, control and infected LNs is shown ((tonsils (N=29), (control LNs (N=29), vir-HIV high-T_{FH} (N=13), vir-HIV low-T_{FH} (N=5), cART HIV high-T_{FH} (N=11) and cART HIV low-T_{FH} (N=7)). (G) Bar graphs showing the mean of minimum distances between CD20^{hi} and PD1^{hi}CD57^{lo} (left) or PD1^{hi}CD57^{hi} (right) T_{FH} cells in tonsils, control and infected LNs (tonsils (N=29), control LNs (N=29), vir-HIV high-T_{FH} (N=13), vir-HIV low-T_{FH} (N=5), cART HIV high-T_{FH} (N=11) and cART HIV low-T_{FH} (N=7)). Each dot represents one follicle in all presented graphs. The p values were calculated using the Mann-Whitney test and were corrected using FDR correction with q=0.05 (Suppl.Table 2).

Then, the aforementioned parameters were calculated for the PD1^{hi}CD57^{lo} and PD1^{hi}CD57^{hi} cells in all tissue groups. Given the low abundancy of CD57^{hi} T_{FH} cells, a significantly lower number of follicular areas, especially in the low-T_{FH} HIV subgroups, was analyzed (Figure 2F and G). Again, a comparable CD20 G-function profile was found among the tissue groups, in these follicular areas (Figure S3A). Our data showed a similar G function and distance profile between tonsils and reactive control LNs (Figure 2F and G). In general, PD1^{hi}CD57^{lo} and PD1^{hi}CD57^{hi} cells express a significantly higher degree of dispersion in HIV infected compared to tonsils and control LNs (Figure 2F). Interestingly, the cART low-T_{FH} subgroup was the one with the highest dispersion of PD1^{hi}CD57^{lo} cells among the PLWH subgroups (Figure 2F). With respect to the mean minimum distance, a trend, which was statistically significant for many of the comparisons, for longer distance between CD20^{hi} and PD1^{hi}CD57^{lo} OR ^{hi} cells was measured in HIV infected compared to tonsils and control LNs (Figure 2G). Our data suggest a distinct profile of the *in situ* T_{FH} cell distribution and neighboring with B cells in PLWH compared to tonsils and control LNs.

3.3. Significant Accumulation of Follicular compared to Extrafollicular FOXP3^{hi} CD4⁺ T Cells in cART low-T_{FH} LNs

We used the expression of FOXP3 as a surrogate for potential immune-regulatory CD4⁺ T cells (Figure 3A). The Histocytometry gating scheme for the identification and calculation of FOXP3^{hi} CD4⁺ T cells in extrafollicular and intrafollicular areas (highly enriched in CD20^{hi/dim} cells) is shown (Figure 3B). The concordance between digitally/Histocytometry identified FOXP3^{hi} CD4^{hi} T cells (shown as spheres) and their original counterparts is demonstrated in Figure 3C. The lowest cell density of extrafollicular (EF) and follicular (F)FOXP3^{hi} CD4⁺ T cells was found in tonsils and the highest in reactive control LNs (Figure 3D and E). Comparable EF-FOXP3^{hi}CD4^{hi} T cell densities among the PLWH subgroups were found (Figure 3D). Although not statistically significant, a trend for higher cell densities of F-FOXP3^{hi} CD4⁺ T cells in cART- compared to vir-HIV LNs was measured (Figure 2E). A broad range of F-FOXP3^{hi} CD4⁺ T cell densities was observed, particularly in the cART low-T_{FH} subgroup (Figure 2E and S3B).

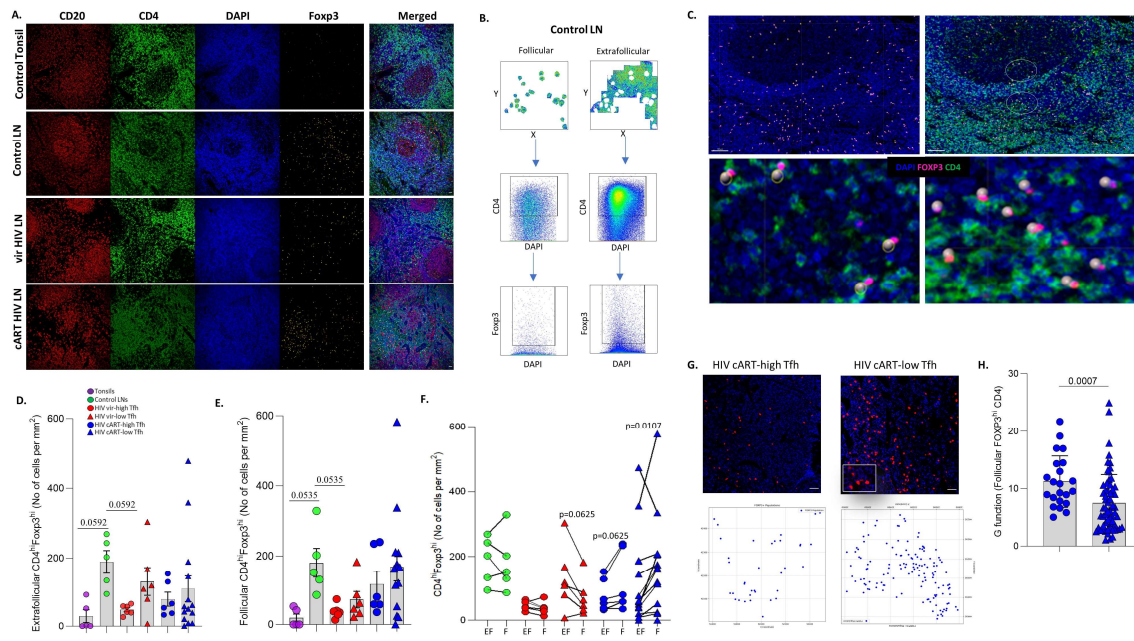


Figure 3. Preferential accumulation of FOXP3^{hi} CD4⁺ T cells in cART HIV follicular areas. (A) Representative examples of CD20(red), CD4 (green), DAPI (blue) and FOXP3 (yellow) staining pattern from a tonsil and control, viremic and cART HIV LNs (scale bar: 30 μ m). (B) Histocytometry immunophenotyping gating strategy used for the sequential identification of FOXP3^{hi} CD4⁺ T cells in follicular and extrafollicular areas in a control LN (C) Representative back gating of Histocytometry identified FOXP3^{hi} CD4⁺ T cells, using Imaris software. Each sphere represents one cell. (D) Bar graph (left) demonstrating the normalised per mm² counts of extrafollicular FOXP3^{hi} CD4⁺ T cells in tonsils (N=5), control LNs (N=5), HIV vir-high-T_{FH} (N=6), HIV vir-low-T_{FH} (N=6), HIV cART-high-T_{FH} (N=6) and HIV cART-low-T_{FH} (N=14). (E) Bar graph showing the normalised per mm² counts of follicular FOXP3^{hi} CD4⁺ T cells in the same tissue samples. Each symbol represents one donor. (F) Bar graph with connecting lines demonstrating the normalised per mm² counts of FOXP3^{hi} CD4⁺ T cells in follicular and extrafollicular regions in each tissue analysed. (G) Representative immunofluorescence images showing the distribution of FOXP3^{hi} (green) and CD20^{hi} (red) cells in follicles from one cART-high-T_{FH} and one cART-low-T_{FH} tissue. The corresponding digitalized (generated by the Python distance analysis script) images are shown too. (H) Bar graph showing the calculated G function values for follicular FOXP3^{hi} CD4⁺ T cells in cART-high T_{FH} (blue circles) and cART-low T_{FH} (blue triangles) (tissues HIV cART-high T_{FH} (N=22) and HIV cART-low T_{FH} (N=64)). The p values were calculated using the Mann-Whitney test and were corrected using FDR correction with q=0.05(Suppl. Table 2).

Next, the EF- and F-FOXP3^{hi} CD4⁺ T cell densities were compared in each LN. Similar EF- and F-FOXP3^{hi} CD4⁺ T cell densities were found in control LNs while fewer F-FOXP3^{hi} CD4⁺ compared to EF-FOXP3^{hi} CD4⁺ T cells were found for almost all viremic PLWH tissues tested (Figure 3F). However, the opposite profile was observed for the cART tissues (Figure 3F). A consistent, significantly higher cell density of F- FOXP3^{hi} CD4⁺ compared to EF-FOXP3^{hi} CD4⁺ T cells was measured, especially in the cART low-T_{FH} subgroup (Figure 3F). The distribution profile (G function) of FOXP3^{hi} CD4⁺ T cells, across the whole imaged area for each tissue, was also investigated. No significant differences were found among the groups analyzed (Figure S3C). Then, we focused our analysis on F-FOXP3^{hi} CD4⁺ T cells. An example of identification and corresponding digital representation of their distribution in cART tissues is shown (Figure 3G). A significantly lower dispersion was measured in cART low-T_{FH} compared to cART high-T_{FH} subgroup, when the G factor was calculated for F-FOXP3^{hi} CD4⁺ T cells (Figure 3H). Our data show a preferential accumulation of follicular immune regulatory CD4 T cells in cART compared to viremic PLWH LNs.

3.4. LN GrzB^{hi}CD8⁺ T Cells Are Negatively Associated with Blood Viral Load

The *in situ* profile of bulk and effector (GrzB^{hi}) CD8⁺ T cells (Figure 4A) was investigated using a multiplex imaging assay and Histocytometry gating scheme is shown in Figure 4B. The applied antibody panel (Supp Table 2, panel II) does not include a follicular/GC biomarker, therefore the cell density of CD8⁺ T cell subsets was analyzed for the whole imaged area (Figure 4A and B). The concordance between digitally/Histocytometry identified GrzB^{hi}CD4^{hi} T cells (shown as spheres) and their original counterparts is demonstrated in Figure 4C. In line with our previous data[15,24], an accumulation of bulk and GrzB^{hi}CD8⁺ T cells was measured in viremic donors, particularly the high-T_{FH} tissues, compared to tonsils and control LNs (Figure 4D and S4A). Although not significant, a reduction of GrzB^{hi}CD8⁺ T cells was observed between the viremic and cART tissues, which was more evident between the high-T_{FH} subgroups (Figure 4D). A positive association between circulating and LN bulk and GrzB^{hi}CD8⁺ T cells was found in HIV viremic samples (Figure S4B). Contrary to circulating CD8⁺ T cells (Figure S4C), a significant negative correlation was observed between the viral load and the LN GrzB^{hi}CD8⁺ T cells (Figure 4E).

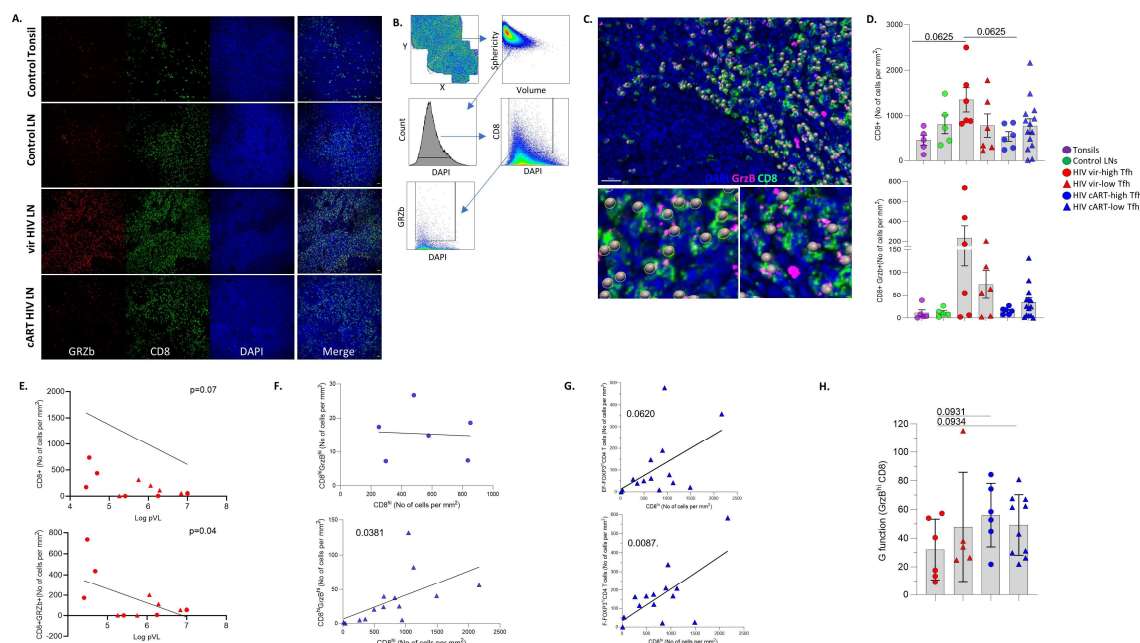


Figure 4. Accumulated LN GrzB^{hi}CD8⁺ T cells are negatively associated with PLWH blood viral load. (A) Representative examples of GRZb (red), CD8 (green) and DAPI (blue) staining pattern from a tonsil and control, vir HIV and cART HIV LNs (scale bar: 30 μ m). (B) Histocytometry gating strategy used for the sequential identification of bulk CD8⁺ and GrzB^{hi}CD8⁺ T cells. (C) Representative back gating of Histocytometry identified GrzB^{hi}CD8⁺ cells using Imaris software. Each sphere represents one cell. (D) Bar graph (upper) demonstrating the normalized per mm² counts of bulk CD8⁺ cells in tonsils (N=5), control LNs (N=5), vir-HIV high-T_{FH} (N=6), vir-HIV low-T_{FH} (N=6), cART HIV high-T_{FH} (N=6) and cART HIV low-T_{FH} (N=14). Bar graph (lower) showing the normalized per mm² counts of GrzB^{hi}CD8⁺ T cells in the same tissue samples. Each symbol represents one donor. (E) Linear regression analysis showing the correlation between LN CD8⁺ (upper panel) and LN GrzB^{hi}CD8⁺ (lower panel) normalized T cell counts with blood viral load. (F) Linear regression analysis showing the correlation between LN CD8⁺ and LN GrzB^{hi}CD8⁺ T cell counts in cART HIV high-T_{FH} (upper panel) and cART HIV low-T_{FH} (lower panel). (G) Linear regression analysis to address the correlation between extrafollicular (upper panel) and follicular (lower panel) FOXP3^{hi}CD4⁺ and LN CD8⁺ normalized T cell counts in cART HIV low-T_{FH} subgroup. (H) Bar graph showing the G function values for the LN GrzB^{hi}CD8⁺ T cells in the HIV subgroups (vir-HIV high-T_{FH} (N=6), vir-HIV low-T_{FH} (N=5), cART HIV high-T_{FH} (N=6) and cART HIV low-T_{FH} (N=10)). The p values were calculated using the Mann-Whitney test and corrected using FDR correction with q=0.05 (Suppl. Table 2).

Next, the correlation between bulk and GrzB^{hi} CD8⁺ as well as FOXP3^{hi} CD4⁺ T cell densities was investigated. A significant association was observed between the two CD8⁺ T cell populations in viremic LNs (Figure S4D) as well as the cART low-T_{FH} subgroup (Figure 4F). However, this was not the case for the cART high-T_{FH} subgroup (Figure 4F). Among the groups analyzed, a positive correlation was found between bulk CD8⁺ T - and EF-FOXP3^{hi} CD4⁺ T cell densities in the cART low-T_{FH} subgroup (Figure 4G, upper panel). This correlation was statistically significant between bulk CD8⁺ T cells and F-FOXP3^{hi} CD4⁺ T cells in the same subgroup (Figure 4G, lower panel). The distance profiling revealed a similar, dispersion of GrzB^{hi} CD8⁺ T cells in LNs from cART compared to those from viremic PLWH (Figure 4H). Conclusively, our data revealed an accumulation of GrzB^{hi} CD8⁺ T cells in PWLH LNs compared to non-infected tissues, which was inversely correlated with the viral load in viremic PLWH.

3.5. Differential Modulation of Innate Immune Cell Subsets by cART

HIV is a chronic disease characterized by immune activation and inflammation[5,36,37]. Given the role of the innate immunity in HIV pathogenesis, we sought to investigate the tissue dynamics of several innate immune cell subsets using relevant biomarkers (CD163 and CD68, markers for monocytes/macrophages[38], CD15, a surrogate for myeloid cells/granulocytes, CD16 a surrogate for activated myeloid cells, neutrophils and NK cells [39,40] (Figure 5A). The Histocytometry gating scheme for the identification and quantification of these cell subsets is shown in Figure 5B. In general, a reduction was measured for all innate immune cell subsets analyzed in low- compared to high-T_{FH} viremic subgroups (Figure 5C), that was significant for the CD15^{hi}CD16^{lo} cells (Figure 5C). With respect to cART, lower cell densities of CD163^{hi}CD68^{lo}, CD15^{hi}CD16^{lo}, CD16^{hi}CD15^{lo} and CD16^{hi}CD15^{hi} cells were found in cART high-T_{FH} compared to viremic high-T_{FH} tissues (Figure 5C). Comparable cell densities of CD68^{hi}CD163^{lo} cells were counted among all tissue groups analyzed (Figure 5C, upper panel).

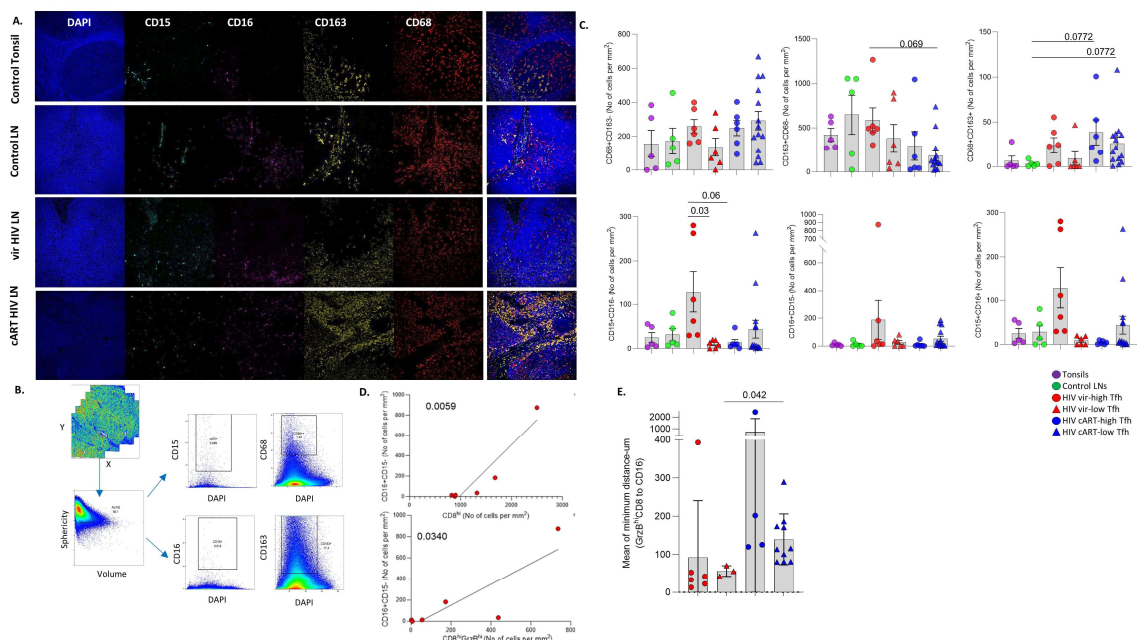


Figure 5. Altered innate immunity signatures among control and HIV samples. (A) Representative examples of DAPI (blue), CD15 (cyan), CD16 (magenta), CD163 (yellow) and CD68 (red) staining pattern from a tonsil and control, vir-HIV and cART-HIV LNs (scale bar: 30 μ m). **(B)** Histocytometry gating strategy used for the sequential identification of CD15^{hi}, CD16^{hi}, CD163^{hi} and CD68^{hi} innate cells. **(C)** Bar graphs demonstrating the normalised per mm² counts of bulk CD68^{hi}CD163^{lo} (upper left), CD68^{lo}CD163^{hi} (upper middle), CD68^{hi}CD163^{hi} (upper right), CD15^{hi}CD16^{lo} (lower left), CD15^{hi}CD16^{lo} (lower middle) and CD15^{hi}CD16^{lo} (lower right) in tonsils (N=5), control LNs (N=5), vir-HIV high-T_{FH} (N=6), vir-HIV low-T_{FH} (N=6), cART HIV high-T_{FH} (N=6) and cART HIV low-T_{FH}

(N=14)). Each symbol represents one donor. **(D)** Linear regression analysis to address the correlation between CD8⁺ (upper panel) or GrzB^{hi}CD8⁺ (lower panel) T cells and CD16^{hi}CD15^{lo} cells in vir-HIV high-T_{FH} tissues. **(E)** Bar graph showing the mean values of the minimum distances between GrzB^{hi}CD8⁺ T and CD16^{hi} cells in tissues from the HIV subgroups vir- HIV high-T_{FH} (N=6), vir-HIV low-T_{FH} (N=3), cART HIV high-T_{FH} (N=4) and cART HIV low-T_{FH} (N=10). Each dot represents a different donor. The p values were calculated using the Mann-Whitney test and p values were corrected using FDR correction with q=0.05 (Suppl.Table 2).

Then, the relationship between CD8⁺ T cells and innate immunity cell types was investigated. A positive association between CD68^{hi} or CD163^{hi} cell subsets and bulk CD8⁺ T cells in viremic LNs was found (Figure S5A). A significant positive correlation between CD16^{hi}CD15^{lo} and bulk or GrzB^{hi}CD8⁺ T cells was found in the vir-HIV high-T_{FH} group (Figure 5D). No such correlations were observed in cART LNs. Similar to GrzB^{hi}CD8⁺ T cells, a significant inverse correlation was also observed between CD16^{hi}CD15^{lo} cells and peripheral blood viral load in viremic PLWH (Figure S5B). Analysis of the in-situ distribution profiling showed a higher dispersion in cART compared to viremic HIV infected tissues for CD163^{hi} cells while comparable profiles were found for CD68^{hi} and CD16^{hi} cells (Figure S5C). Furthermore, a lower minimum mean distance between GrzB^{hi}CD8⁺ and CD16^{hi} cells, but not CD68^{hi} or CD163^{hi}, in viremic compared to cART HIV tissues was found (Figure 5E and S5D). Altogether, our data suggest that cART has a differential impact on the cell density of individual innate immunity cell subsets.

4. Discussion

Here, we have investigated the immune landscaping in reactive LNs from PLWH and compared it non-infected, control LNs and tonsils (Figure S6). We chose to compare the *in situ* immune dynamics in HIV LNs to non-infected, reactive LNs characterized by active follicles (follicular hyperplasia), as a reference for highly active F/GCs. Given the abundance in GC B and T_{FH} cells as well as the preservation of the follicular and sub-follicular structures tonsils are considered as a 'prototype' lymphoid organ for the investigation of F/GC immune cell types. We should emphasize that none of the viremic PLWH had active opportunistic infections or AIDS-defining pathologies at the time of the sampling. The time since diagnosis was also similar among the individuals. Our analysis revealed two subgroups of HIV infected LNs with respect to the cell density of T_{FH} cells, in both viremic and cART PLWH. This profile, at least for viremic individuals, is in line with the T_{FH} cell dynamics in SIV non-human primate model[10,11].

No association of T_{FH} cell densities with gender, age, CD4⁺ and CD8⁺ counts was found in both viremic and cART PLWH. HIV infection of LN CD4⁺ T cells *per se*, intrinsic factors and/or the interaction of T_{FH} cells with the GC microenvironment represent potential mechanisms that could contribute to T_{FH} cell in-situ dynamics by altering the differentiation and/or turnover rate of total (or specific subsets) of T_{FH} cells in PLWH. Regarding the viremic PLWH, we observed a negative association between pVL and GC/T_{FH} cells that could reflect a preferential infection/loss of T_{FH} cells or a generalized loss of T_{FH} cells in highly viremic PLWH. The relatively low numbers (~5% of T_{FH} cells) of HIV DNA⁺ T_{FH} cells [9] are challenging the impact of the productive HIV infection *per se*. Similar infection rates for CD57^{hi} and CD57^{lo} T_{FH} cells have been reported previously[41] challenging the preferential infection/loss of CD57^{hi} T_{FH} cells and the observed weaker association between these two T_{FH} cell subsets in viremic compared to cART PLWH. Abortive HIV infection represents an alternative mechanism for the loss of tonsillar CD4 T cells at least *in vitro* [42]. The role of such mechanism for the regulation of vir-HIV T_{FH} cells needs to be investigated. Alternatively, progressive fibrosis and damage of vital LN structural elements (e.g. the Fibroblastic Reticular Cell network[43] and/or loss of GC survival signals (e.g. due to damage of the Follicular Dendritic Cell network[44] for T_{FH} cells in highly vireemics could affect the differentiation and maintenance or turnover of T_{FH} cells. The observed heterogeneity of T_{FH} cell densities in different follicles across an individual tissue indicates that the locality of such mechanisms is possibly an important factor to consider in future studies. Our data urge for further investigation of LN structure elements in conjunction with the in-

situ dynamics of immune cell types. The development of appropriate imaging tools will greatly facilitate such efforts.

Two groups (LoViReT and HiViReT) of treated PLWH, harboring a relatively wide range of very low viral reservoir, was recently described [45]. Whether the cART T_{FH} subgroups correspond to a status is not known and merits further investigation. Despite the viral control, cART is not able to fully restore the LN/follicular damage in PLWH back to normal. FRC reconstitution is one of the factors that could affect the reconstitution of LN CD4⁺ T cell pool and presumably the T_{FH} cell prevalence[46]. No association of T_{FH} cell densities with treatment duration was found. However, the capacity of individual PLWH to differentially respond to cART and restore relevant LN elements could contribute to the observed high- and low-T_{FH} subgroups in the cART HIV group. Our distribution analysis showed an overall higher dispersion of the PD1^{hi} T_{FH} cells in HIV infected compared to non-infected tissues, that is also associated with a longer mean distance between T_{FH} and B cells in the infected donors. A mutual regulation between T_{FH} and GC B cells has been reported previously[47]. We hypothesize that the described spatial distribution profile may reflect a lower probability for these two cell subsets to interact in the infected LNs leading to the subsequent loss of vital signals for T_{FH} cells. The aforementioned profile was more evident in the low-T_{FH} HIV subgroups, further supporting our hypothesis.

Follicular immune-regulatory CD4⁺ T cells (T_{FR}) represent an important 'microenvironment cell factor' for the development of T_{FH} cells[14,48,49]. Tonsils harbor the lowest number of FOXP3^{hi} CD4⁺ T cells, in line with previous reports[48,50]. Our data revealed a contrasting profile regarding the cell density between EF- and F-FOXP3^{hi} CD4⁺ T cells in control and viremic compared to cART-HIV LNs. Within the cART HIV group, we measured a significant increase of F-FOXP3^{hi} CD4⁺ T specifically in the cART-low T_{FH} subgroup, suggesting a negative role for the T_{FH} cell development in these individuals. Supplementary to this is the significantly less scattered distribution of the FOXP3^{hi} CD4⁺ T cells within the follicles of low- compared to high-T_{FH} cART tissues. Whether the FOXP3^{hi} CD4⁺ T cells represent bona fide T_{FR} cells or cells originated from T_{FH} cells[51] is not known and needs further investigation. Our data urge for a comprehensive *in situ* phenotypic and functional characterization of FOXP3^{hi} CD4⁺ T cells, especially in cART-HIV PLWH.

In contrast to PLWH, the majority of follicular CD8⁺ T cells in tonsils and control LNs express a GrzB^{lo} phenotype, in line with our previous observation[24]. The positive association between the numbers of circulating and LN CD8⁺ T cell density suggests that increased trafficking of bulk and presumably effector CD8⁺ T cells may support, at least in part, their increased cell density in viremic LNs. A CXCR3/CXCR3L mediated mechanism, that has been previously proposed HIV PLWH[52] and SIV infected non-human primates[15], could contribute to the CD8⁺ T cell density profile we observed for viremic PLWH. Several studies have shown the role of CD8⁺ T cells in controlling HIV and SIV[53,54]. In line with these studies, we found a negative correlation between LN CD8⁺ and GrzB^{hi} CD8⁺ with pVL that indicates a potential role of CD8⁺ T cells for viral control, at least in part, in our cohort. The reduction of GrzB^{hi} CD8⁺ T cells in cART-HIV LNs, particularly in the high-T_{FH} subgroup, could reflect a lower immune activation due to therapy, in line with the overall lower cell density of several innate immunity cell subsets observed in cART-HIV. Further comprehensive *in situ* phenotypic (e.g. expression of homing receptors), functional (e.g. 'regulatory' function [55]) and topological characterization of CD8⁺ T cells, especially in cART-HIV PLWH, is of great interest given their potential role for immunotherapies aiming to eliminate the virus. We found a positive correlation between CD8⁺ and F-FOXP3^{hi} CD4⁺ T cells specifically in the low-T_{FH} cART-HIV subgroup. Whether and how these two cell types could affect the cell density of T_{FH} cells in this group remains to be elucidated.

Overall, we observed a diverse profile of innate immunity cell types among the groups. Individual cell types were differentially modulated by cART while no consistent association with the low- or high-T_{FH} status was observed. We measured different cell densities for the CD68^{hi}CD163^{hi} and CD68^{lo}CD163^{hi} cell subsets. CD163 is a receptor that can be cleaved and therefore the cell density of CD163^{hi} macrophages/monocytes can be underestimated. Our results, however, indicate that possible cleavage/loss of CD163 is not responsible for the observed in-situ dynamics [44]. Our data point to a

diverse innate immunity LN microenvironment that could affect the host-virus interplay in these LNs [18]. We found a strong correlation between LN CD8+ T cells and CD16^{hi}CD15^{lo} cells in high-T_{FH} viremic tissues. This profile was also associated with i) a less dispersed CD8+ T cells distribution, ii) a shorter distance between CD8+ and CD16^{hi} cells and iii) a negative association between pVL and LN CD8+ or CD16^{hi}CD15^{lo} cells. These findings urge for further investigation of neutrophils/granulocytes, in addition to macrophages, as possible key determinants for the innate immunity / CD8+ T cell cross talk and virus dynamics[56]. Whether the same or different innate immune cell subsets mediate the host-virus interaction in viremic and cART PLWH is not known and remains to be elucidated.

Altogether, we have analyzed several immunological cell types in a well characterized cohort of LNs and provide evidence i) for the subgrouping of HIV-infected LNs (both from viremic and cART PLWH) based on their T_{FH} cell density, ii) of a distinct profile of potential immunosuppressive FOXP3^{hi} CD4+ T cells in cART LNs with respect to their cell densities, distribution between extrafollicular and follicular areas, and spatial distribution within the follicular compartment and iii) the effect of cART on the cell density of CD8+ T and innate immune cells (Table 2). Altered T_{FH} cell density in HIV subgroups is associated with different CD8+ and F-FOXP3^{hi} CD4+ T cell density and distribution profiles too. The data suggest that further investigation of CD8 and immune-regulatory CD4 T cells could provide insights for the T_{FH} cell prevalence in HIV and particularly in cART PLWH. Understanding the follicular/GC microenvironment in HIV infection could further inform for the role of T_{FH} cells in HIV pathogenesis and for possible combinatorial interventions aiming to manipulate a major HIV tissue reservoir.

Table 1. Demographic and clinical information of study PLWH.

ID (cART-HIV)	Age	Gender	Anatomic location	CD4+ counts (cells/uL)	HIV RNA copies/mL	Yrs HIV+	Treatment Duration	CurrentART Regimen
cART-LN1	52	M	Inguinal	708	ND	6.5	5	EVG/COBI/3TC/TAF
cART-LN2	60	M	Inguinal	864	ND	22	22	DTG/DESCOVY
cART-LN3	56	F	Inguinal	437	ND	23	15	DTG/DESCOVY
cART-LN4	67	F	Inguinal	1168	ND	10	7.5	Biktarvy
cART-LN5	53	F	Inguinal	454	ND	26	11	Triumeq
cART-LN6	53	M	Inguinal	271	ND	9	14	DVC/COBI/TRV
cART-LN7	50	M	Inguinal	849	ND	32	15	Genvova
cART-LN8	59	M	Inguinal	587	ND	10	10	Atripla
cART-LN9	63	M	Inguinal	276	<40	14	4	RPV/DRV/RTV/DTG
cART-LN10	52	M	Inguinal	459	ND	13	1	ABC/3TC/DTG
cART-LN11	46	M	Inguinal	493	ND	3	3	EVT/COBI/3TC/TDF
cART-LN12	65	M	Inguinal	476	ND	26	25	FPV/RTV/3TC/TDF/M VC
cART-LN13	54	F	Inguinal	459	ND	13	1	ABC/3TC/DTG
cART-LN14	44	M	Inguinal	545	ND	16	7	ATV/RTV/FTC/TDF
cART-LN15	33	M	Inguinal	1121	ND	3y5mo	2y 1mo	EVG/COBI/FTC/TDF
cART-LN16	51	M	Inguinal	805	ND	17	10	DTG/FTC/TDF
cART-LN17	37	M	Inguinal	662	ND	5	4	EFV/FTC/TDF
cART-LN18	53	M	Inguinal	441	ND	22	10	DTG/FTC/TDF
cART-LN19	57	M	Inguinal	500	<40	29	17	DRV/RTV/ABC/FTC/T DF
cART-LN20	58	M	Inguinal	636	ND	19	15	DRV/RTV/FTC/TDF
ID (viremic-HIV)	Age	Gender	Anatomic location	CD4+ counts (cells/uL)	CD8+ counts (cells/uL)	Treatment Duration	LogpVL	
HIV-LN1	27	M	Cervical	520	175	No treatment	5.26	
HIV-LN2	20	M	Cervical	290	881	No treatment	7	
HIV-LN3	29	M	Inguinal	545	830	No treatment	5.41	
HIV-LN4	22	M	Cervical	476	465	No treatment	5.75	
HIV-LN5	37	M	Inguinal	391	1158	No treatment	6.25	
HIV-LN6	24	M	Inguinal	453	3623	No treatment	6.84	
HIV-LN7	29	M	Cervical	347	756	No treatment	7	
HIV-LN8	33	M	Cervical	499	2211	No treatment	6.06	

HIV-LN9	31	M	Inguinal	281	2142	No treatment	6.29
HIV-LN10	35	M	Cervical	491	2284	No treatment	4.49
HIV-LN11	27	M	Cervical	719	1831	No treatment	4.69
HIV-LN12	28	M	Cervical	777	2195	No treatment	4.49
ID (reactive LNs)		Age	Gender	Anatomic location			
LN1		74	M	Axillary			
LN2		41	M	Cervical			
LN3		21	F	Cervical			
LN4		49	M	Inguinal			
LN5		25	F	Inguinal			

Table 2. A table summarizing the main comparisons for immune cell subsets among the tissue groups.

	T _{FH} PD1 ^{hi}	T _{FH} PD1 ^{hi} CD57 ^{hi}	FOXP3 ^{hi} CD4 ⁺ (Follicular)	CD8 ⁺ (total tissue)	GrzB ^{hi} CD8 ⁺ (total tissue)	CD68 ⁺ CD163 ⁻ (total tissue)	CD68 ⁻ CD163 ⁺ (total tissue)	CD15 ⁺ CD16 ⁻ (total tissue)	CD15 ⁻ CD16 ⁺ (total tissue)
Tonsils	++	++	-/+	+	-/+	+	++	-/+	-
control LNs	+++	+++	++	+	-/+	+	++	-/+	-/+
viremic HIV	+ / ++	+	+	+ / ++	++ / +++	+	++	- / ++	-
cART HIV	+ / ++	+	+ / ++	+	+ / ++	+	+ / ++	- / +	-

Supplementary Materials: The following supporting information can be downloaded at the website of this paper posted on Preprints.org.

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Institutional Review Board Statement: All procedures were in accordance with the Declaration of Helsinki and approved by the appropriate Institutional Review Board/Ethical Committee. The utilization of these samples was formally sanctioned by both the Research Committee and the Ethics in Research Committee of the National Institute of Respiratory Diseases "Ismael Cosío Villegas," Mexico City as part of the "C71-18" protocol, ii) University of Washington (study ID: STUDY00001091, CR ID:CR00004042) and iii) the Canton de Vaud-CER-VD, Switzerland for LNs (2021-01161) and tonsils (PB_2016-02436 (201/11)). Written informed consent was obtained from all participants.

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Data Sharing Statement: The authors agree to share all publication-related data. For further information, please contact the corresponding author at Konstantinos.Petrovas@chuv.ch.

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